GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 6, 2004, 19:23:00 ; Search time 75.1875 Seconds
(without alignments)
28.627 Million cell updates/sec

Title: US-10-618-644-3
Perfect score: 38
Sequence: 1 NWGPLV 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	38	100.0	6	5	ABB81805	Abb81805 Soybean a
2	38	100.0	561	1	AAP61363	Aap61363 Soybean g
3	38	100.0	562	5	ABG71268	Abg71268 Glycine m
4	38	100.0	562	7	ADH89249	Adh89249 G. max gl
5	38	100.0	562	7	ADL90188	Ad190188 Soybean g
6	38	100.0	562	8	ADG43984	Adg43984 G. max gl
7	36	94.7	791	6	ABU16711	Abu16711 Protein e
8	36	94.7	798	6	ADA33211	Ada33211 Acinetoba
9	35	92.1	611	4	ABB53092	Abb53092 Escherich
10	34	89.5	51	5	ABP04775	Abp04775 Human ORF
11	34	89.5	59	4	AAO12092	Aao12092 Human pol
12	34	89.5	219	7	ADM04268	Adm04268 Human pro
13	34	89.5	250	5	ABB91948	Abb91948 Herbicida
14	34	89.5	267	3	AAG43748	Aag43748 Arabidops
15	34	89.5	272	3	AAG23820	Aag23820 Arabidops
16	34	89.5	272	3	AAG53364	Aag53364 Arabidops
17	34	89.5	286	3	AAG43747	Aag43747 Arabidops
18	34	89.5	293	3	AAG23819	Aag23819 Arabidops
19	34	89.5	293	3	AAG53363	Aag53363 Arabidops
20	34	89.5	340	3	AAG43746	Aag43746 Arabidops
21	34	89.5	367	3	AAG53362	Aag53362 Arabidops
22	34	89.5	367	3	AAG23818	Aag23818 Arabidops
23	34	89.5	367	5	ABB90886	Abb90886 Herbicida
24	34	89.5	441	2	AAR22000	Aar22000 Partial M
25	34	89.5	564	8	ADJ35072	Adj35072 Xylanase
26	34	89.5	629	4	ABB64027	Abb64027 Drosophil
27	34	89.5	629	4	AAE00297	Aae00297 Drosophil
28	34	89.5	646	6	ABU70925	Abu70925 Human adi
29	34	89.5	646	7	ADD47489	Add47489 Human Pro
30	34	89.5	690	6	ABJ25405	Abj25405 Aspergill
31	34	89.5	793	6	ABJ26005	Abj26005 Aspergill
32	34	89.5	801	4	ABG09122	Abg09122 Novel hum
33	34	89.5	801	4	ABG10073	Abg10073 Novel hum
34	34	89.5	889	4	ABG06563	Abg06563 Novel hum
35	34	89.5	1114	2	AAR21999	Aar21999 M17 antig
36	33	86.8	27	6	ABJ19686	Abj19686 Human sec
37	33	86.8	27	6	ABP99591	Abp99591 Human sec
38	33	86.8	27	6	ABR01074	Abr01074 Human gen
39	33	86.8	27	7	ADC20402	Adc20402 Human sec
40	33	86.8	28	4	AAB64902	Aab64902 Human sec
41	33	86.8	51	5	ABP01920	Abp01920 Human ORF
42	33	86.8	86	5	ABP06347	Abp06347 Human ORF
43	33	86.8	89	4	AAB72464	Aab72464 Human NP5
44	33	86.8	93	2	AAR96579	Aar96579 Monoclona
45	33	86.8	220	5	ABP02586	Abp02586 Human ORF

ALIGNMENTS

RESULT 1
ABB81805
ID ABB81805 standard; peptide; 6 AA.
XX
AC ABB81805;
XX
DT 23-SEP-2002 (first entry)
XX
DE Soybean angiotensin converting enzyme inhibitory peptide #3.
XX
KW Soybean; angiotensin converting enzyme inhibitor; hypertension;
KW hypotensive; taste.
XX
OS Glycine max.
XX
PN WO200255546-A1.
XX
PD 18-JUL-2002.
XX
PF 15-JAN-2002; 2002WO-JP000194.
XX
PR 16-JAN-2001; 2001JP-00007400.
PR 04-OCT-2001; 2001JP-00308974.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Kodera T, Nio N;
XX
DR WPI; 2002-520117/55.
XX
PT Peptides, useful as hypotensive agents or in health foods.
XX
PS Claim 1; Page 19; 43pp; Japanese.
XX
CC The invention relates to a novel set of peptides and their salts. The
CC peptides of the invention have hypotensive activity. The peptides are
CC used as hypotensive agents or in health foods, and have favourable taste.
CC The present sequence represents a peptide of the invention, having
CC angiotensin converting enzyme inhibitory activity
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 38; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NWGPLV 6
||||||

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Db          1 NWGPLV 6


RESULT 2
AAP61363
ID   AAP61363 standard; protein; 561 AA.
XX
AC   AAP61363;
XX
DT   25-MAR-2003  (revised)
DT   16-OCT-1991  (first entry)
XX
DE   Soybean glycinin A5A4B3 subunit.
XX
KW   Soybean protein; glycinin.
XX
OS   Glycine max.
XX
PN   JP61132189-A.
XX
PD   19-JUN-1986.
XX
PF   03-DEC-1984;   84JP-00254217.
XX
PR   03-DEC-1984;   84JP-00254217.
XX
PA   (NORQ ) NORINSHO KK.
XX
DR   WPI; 1986-200545/31.
DR   N-PSDB; AAN60940.
XX
PT   Prepn. of soybean messenger RNA - for insertion into cells or
PT   microorganisms to produce soybean protein.
XX
PS   Example 2; Fig 2; 7pp; Japanese.
XX
CC   Sequence derived from mRNA may be used for the expression of the soybean
CC   protein by a foreign host. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 561 AA;

  Query Match             100.0%;  Score 38;  DB 1;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NWGPLV 6
              ||||||
Db        542 NWGPLV 547


RESULT 3
ABG71268
ID   ABG71268 standard; protein; 562 AA.
XX
AC   ABG71268;
XX
DT   17-DEC-2002  (first entry)
XX
DE   Glycine max (Soybean) cv. forrest protein.
XX
KW   Soybean; Glycinin; atomic coordinate data; processability; soya protein;
KW   forrest; protein co-ordinate data.
XX
OS   Glycine max.
XX
PN   JP2002193996-A.
XX
PD   10-JUL-2002.
XX
PF   21-DEC-2000; 2000JP-00405097.
XX
PR   21-DEC-2000; 2000JP-00405097.
XX
PA   (KYOU ) UNIV KYOTO.
XX
DR   WPI; 2002-685438/74.
DR   N-PSDB; ABS55195.
XX
PT   Glycinin, beta-conglycinin and proglycinin, their crystal structures,
PT   three dimensional coordinates, three dimensional structured and models
PT   and their uses.
XX
PS   Disclosure; Page 1280-1282; 1298pp; Japanese.
XX
CC   The present invention relates to a new Glycinin characterised by the
CC   atomic coordinate data fully defined in the specification. The structure
CC   can be used for improving processability of soya protein. The present
CC   amino acid sequence represents the Glycine max (Soybean) cv. forrest
CC   protein, as described in the specification
XX
SQ   Sequence 562 AA;

  Query Match             100.0%;  Score 38;  DB 5;  Length 562;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NWGPLV 6
              ||||||
Db        543 NWGPLV 548


RESULT 4
ADH89249
ID   ADH89249 standard; protein; 562 AA.
XX
AC   ADH89249;
XX
DT   06-MAY-2004  (first entry)
XX
DE   G. max glycinin A5A4B3 subunit.
XX
KW   double stranded RNA; storage protein; 2S-albumen; 7S-globulin;
KW   11S/12S-globulin; zein-prolamine; homogentistate metabolic pathway;
KW   pharmaceutical; plant; abiotic stress; fatty acid composition;
KW   lipid composition; oil composition; carbohydrate composition; colour;
KW   pigmentation; pathogen resistance; fruit ripening delay; aging;
KW   male sterility; lignin; fibre; cotton; Vitamin E synthesis; nicotine;
KW   caffeine; theophylline; threonine biosynthesis; glycinin.
XX
OS   Glycine max.
XX
PN   WO2003078629-A1.
XX
PD   25-SEP-2003.
XX
PF   17-MAR-2003; 2003WO-EP002735.
XX
PR   20-MAR-2002; 2002DE-01012892.
XX
PA   (BADI ) BASF PLANT SCI GMBH.
XX
PI   Kock M,  Bauer J;
XX
DR   WPI; 2003-803889/75.
DR   N-PSDB; ADH89248.
XX
PT   Reducing expression of at least two target genes, useful e.g. for
PT   producing transgenic plants, using partly double-stranded interfering
PT   RNA.
XX
PS   Disclosure; SEQ ID NO 24; 228pp; German.
XX
CC   This invention describes a novel method for reducing the expression of at
CC   least two different endogenous target genes in a eukaryotic cell or
CC   organism by introducing an RNA molecule that is at least partly double
CC   stranded. The transcribed RNAs from at least two target genes have
```

CC homology below 90% and the RNA molecule is formed as a single, self-
CC complementary molecule. At least one of the double-stranded structures
CC formed from individual sense sequences has an even number of repeats of
CC 21 or 22 bp. The RNA molecule may include an intron-encoding sequence. At
CC least two target genes are selected from different classes of storage
CC protein genes, i.e. 2S-albumen, 7S- or 11S/12S-globulins or zein-
CC prolamine and at least one of the sense sequences is identical to storage
CC protein sequences or genes in the homogentistate metabolic pathway or
CC enzyme types, e.g. acetyl transacylases, thioesterases, (de)branching
CC enzymes or cellulases. The RNA of the invention, also related cassettes,
CC expression systems, vectors and transgenic organisms are used for
CC preparation of pharmaceuticals, in biotechnological processes and plant
CC biotechnology, specifically in plants to improve protection against
CC abiotic stress, to modify composition and/or content of fatty acids,
CC lipids and oils, to modify carbohydrate composition, to alter colour or
CC pigmentation, to reduce content of storage proteins, to increase
CC resistance to pathogens, to inhibit stem break, to delay fruit ripening
CC or aging, to induce male sterility, to reduce content of toxic or
CC unwanted components, to modify lignification and/or lignin content, to
CC modify the fibre component in foods or fibre quality in cotton, to reduce
CC susceptibility to shock, to increase synthesis of Vitamin E, to reduce
CC contents of nicotine, caffeine or theophylline and to increase methionine
CC content, by reducing threonine biosynthesis. The method provides a rapid
CC and efficient way of reducing gene expression, can inhibit more than one
CC target gene, prevents development of multiple phenotypes (since the
CC transcription rate is the same for all RNA sequences, significantly
CC reducing the selection process required to produce an organism with
CC effective suppression of all target genes), avoids problems of epigenic
CC gene silencing, does not require synthesis of individual RNA sequences
CC and the method can be applied to plants with complex (polyploid) genomes.
CC No interference between the individual RNA sequences occur. This sequence
CC represents a protein encoded by a target gene used in the method of the
CC invention.
XX
SQ Sequence 562 AA;

Query Match 100.0%; Score 38; DB 7; Length 562;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NWGPLV 6
||||||
Db 543 NWGPLV 548

RESULT 5
ADL90188
ID ADL90188 standard; protein; 562 AA.
XX
AC ADL90188;
XX
DT 20-MAY-2004 (first entry)
XX
DE Soybean glycinin G4 protein.
XX
KW immunomodulator; immunotherapy; allergen characterisation;
KW immunoglobulin E; allergen sensitivity; soybean; glycinin G4;
KW acidic protein.
XX
OS Glycine max.
XX
PN US2003166518-A1.
XX
PD 04-SEP-2003.
XX
PF 12-JAN-2001; 2001US-00759967.
XX
PR 13-JAN-2000; 2000US-0175948P.
PR 03-MAR-2000; 2000US-0186724P.
XX
PA (BEAR/) BEARDSLEE T A.
PA (ZEEC/) ZEECE M G.
PA (SARA/) SARATH G.
PA (MARK/) MARKWELL J P.
XX
PI Beardslee TA, Zeece MG, Sarath G, Markwell JP;
XX
DR WPI; 2003-898094/82.
XX
PT Allergen characterization comprises obtaining a recombinant fusion
PT protein and detecting the binding of immunoglobulin E molecules in the
PT biological sample to the recombinant fusion protein.
XX
PS Disclosure; SEQ ID NO 22; 34pp; English.
XX
CC The invention describes a method of allergen characterisation comprising:
CC obtaining a recombinant fusion protein; attaching the recombinant fusion
CC protein to a substrate through the native protein; contacting the
CC recombinant fusion protein attached to the substrate with a biological
CC sample from an individual; and detecting the binding of immunoglobulin E
CC molecules in the biological sample to the recombinant fusion protein.
CC Also described are: a method for determining the sensitivity of an
CC individual to a suspected allergen; a method for determining the amount
CC of immunoglobulin E specific for an allergen in a biological sample; a
CC method of immunotherapy; a method of allergen characterisation; a method
CC for determining the sensitivity of an individual to a suspected allergen;
CC a method of determining the amount of immunoglobulin E specific for an
CC allergen in a biological sample; a kit comprising the recombinant fusion
CC protein and instructions for using the recombinant fusion protein to
CC determine IgE binding to the know or suspected allergen; and a method for
CC epitope determination. The method is useful for characterising allergens.
CC This is the amino acid sequence of soybean glycinin G2 acidic protein
CC that can be used to demonstrate the methods of the invention.
XX
SQ Sequence 562 AA;

Query Match 100.0%; Score 38; DB 7; Length 562;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NWGPLV 6
||||||
Db 543 NWGPLV 548

RESULT 6
ADG43984
ID ADG43984 standard; protein; 562 AA.
XX
AC ADG43984;
XX
DT 26-FEB-2004 (first entry)
XX
DE G. max glycinin A5A4B3 subunit protein.
XX
KW oil content; plant; storage protein; seed-specific promoter; 2S-albumin;
KW 7S-globulin; 11S-globulin; 12S-globulin; zein-prolamine; transgenic;
KW oil production; fat production; free fatty acid production; food;
KW animal feed; pharmaceutical; fine chemical production; glycinin.
XX
OS Glycine max.
XX
PN WO2003077643-A2.
XX
PD 25-SEP-2003.
XX
PF 17-MAR-2003; 2003WO-EP002733.
XX
PR 20-MAR-2002; 2002DE-01012893.
XX
PA (BADI) BASF PLANT SCI GMBH.
XX
PI Bauer J;
XX
DR WPI; 2004-011485/01.
DR N-PSDB; ADG43983.

```
XX
PT   Increasing total oil content of plants, useful e.g. as foods or animal
PT   feeds, by reducing amount of storage proteins, particularly with double-
PT   stranded interfering RNA.
XX
PS   Claim 4; SEQ ID NO 24; 253pp; German.
XX
CC   This invention describes a novel method for increasing the total oil
CC   content of a plant by reducing the amount of at least one storage protein
CC   in the plant (or its tissue, organs, parts or cells) and selecting plants
CC   that have higher total oil content than starting plants. The storage
CC   protein is suppressed by introducing antisense RNA, optionally combined
CC   with a ribozyme, sense RNA that induces co-suppression, DNA-binding
CC   factors directed against storage protein genes, viral sequences that
CC   degrade storage protein RNA, constructs that induce homologous
CC   recombination of endogenous storage protein genes or mutations into
CC   storage protein genes. Most preferably a plant cell is stably transfected
CC   with a recombinant expression construct, then regenerated to plants that
CC   express the incorporated sequence. The expression constructs particularly
CC   contain a seed-specific promoter and they are introduced into plants by
CC   standard methods, e.g. via Agrobacterium. The preferred storage proteins
CC   of the invention are 2S-albumens, 7S or 11S/12S-globulins or zein-
CC   prolamines. Transgenic organisms produced by the new method are used for
CC   production of oils, fats, free fatty acids or their derivatives, useful
CC   as foods, animal feeds, pharmaceuticals and fine chemicals. This sequence
CC   represents a storage protein used to illustrate the method of the
CC   invention.
XX
SQ   Sequence 562 AA;

  Query Match             100.0%;  Score 38;  DB 8;  Length 562;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NWGPLV 6
              ||||||
Db        543 NWGPLV 548


RESULT 7
ABU16711
ID   ABU16711 standard; protein; 791 AA.
XX
AC   ABU16711;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Protein encoded by Prokaryotic essential gene #2238.
XX
KW   Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS   Acinetobacter baumannii.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Wang L,  Zamudio C,  Malone C,  Haselbeck R,  Ohlsen KL,  Zyskind JW;
PI   Wall D,  Trawick JD,  Carr GJ,  Yamamoto R,  Forsyth RA,  Xu HH;
XX
DR   WPI; 2003-029926/02.
DR   N-PSDB; ACA20581.
XX
PT   New antisense nucleic acids, useful for identifying proteins or screening
PT   for homologous nucleic acids required for cellular proliferation to
PT   isolate candidate molecules for rational drug discovery programs.
XX
PS   Claim 25; SEQ ID NO 44635; 1766pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising any one of
CC   the 6213 antisense sequences given in the specification where expression
CC   of the nucleic acid inhibits proliferation of a cell. Also included are:
CC   (1) a vector comprising a promoter operably linked to the nucleic acid
CC   encoding a polypeptide whose expression is inhibited by the antisense
CC   nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC   polypeptide or its fragment whose expression is inhibited by the
CC   antisense nucleic acid; (4) an antibody capable of specifically binding
CC   the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC   proliferation or the activity of a gene in an operon required for
CC   proliferation; (7) identifying a compound that influences the activity of
CC   the gene product or that has an activity against a biological pathway
CC   required for proliferation, or that inhibits cellular proliferation; (8)
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
CC   or a gene on which the test compound that inhibits proliferation of an
CC   organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC   compound's activity; (11) a culture comprising strains in which the gene
CC   product is overexpressed or underexpressed; (12) determining the extent
CC   to which each of the strains is present in a culture or collection of
CC   strains; or (13) identifying the target of a compound that inhibits the
CC   proliferation of an organism. The antisense nucleic acids are useful for
CC   identifying proteins or screening for homologous nucleic acids required
CC   for cellular proliferation to isolate candidate molecules for rational
CC   drug discovery programs, or for screening homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC   the target prokaryotic essential genes. Note: The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 791 AA;

  Query Match             94.7%;  Score 36;  DB 6;  Length 791;
  Best Local Similarity   83.3%;  Pred. No. 6.3e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NWGPLV 6
              ||||:|
Db         88 NWGPIV 93


RESULT 8
ADA33211
ID   ADA33211 standard; protein; 798 AA.
XX
AC   ADA33211;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Acinetobacter baumannii protein #372.
XX
KW   Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
KW   plant biocontrol agent.
XX
OS   Acinetobacter baumannii.
XX
PN   US6562958-B1.
XX
PD   13-MAY-2003.
XX
PF   04-JUN-1999;   99US-00328352.
XX
PR   09-JUN-1998;   98US-0088701P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
```

XX
PI Breton G, Bush D;
XX
DR WPI; 2003-576092/54.
DR N-PSDB; ADA29085.
XX
PT New Acinetobacter baumanii proteins and nucleic acids, useful as reagents
PT for diagnosing a bacterial disease, as components of antibacterial
PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for
PT plants.
XX
PS Example; SEQ ID NO 4498; 328pp; English.
XX
CC The invention relates to isolated Acinetobacter baumannii nucleic acids.
CC The A. baumannii nucleic acids and polypeptides are useful as reagents
CC for diagnosing a bacterial disease, as components of antibacterial
CC vaccines, as targets for antibacterial drugs, to detect the presence of
CC A. baumannii and other Acinetobacter species in a sample, in screening
CC compounds for the ability to interfere with the A. baumannii life cycle
CC or to inhibit A. baumannii infection, and as biocontrol agents for
CC plants. The present sequence represents the amino acid sequence of an A.
CC baumannii protein.
XX
SQ Sequence 798 AA;

Query Match 94.7%; Score 36; DB 6; Length 798;
Best Local Similarity 83.3%; Pred. No. 6.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NWGPLV 6
||||:|
Db 95 NWGPIV 100

RESULT 9
ABB53092
ID ABB53092 standard; protein; 611 AA.
XX
AC ABB53092;
XX
DT 11-FEB-2002 (first entry)
XX
DE Escherichia coli polypeptide SEQ ID NO 1566.
XX
KW Escherichia coli; B2/D+A-; antiinflammatory; antibacterial;
KW immunosuppressive; extra-intestinal infection; phylogeny; meningitis;
KW systemic infection; non-diarrhoeal infection; septicaemia;
KW pyelonephritis; antibiotic resistance.
XX
OS Escherichia coli.
XX
PN WO200166572-A2.
XX
PD 13-SEP-2001.
XX
PF 12-MAR-2001; 2001WO-EP003445.
XX
PR 10-MAR-2000; 2000FR-00003145.
PR 02-FEB-2001; 2001FR-00001449.
XX
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Bingen E, Bonacorsi S, Clermont O, Nassif X, Tinsley C;
XX
DR WPI; 2001-550253/61.
XX
PT A library of DNA fragments of Escherichia coli strains for the phylogenic
PT determination of a given strain comprises polynucleotides of nature B2/D+
PT A-.
XX
PS Example 6; Fig 6; 646pp; English.
XX
CC The invention relates to a library of DNA fragments of Escherichia coli
CC strains comprising polynucleotides (ABA88577-ABA88729 and ABA89533) and
CC encoded proteins (ABB52459-ABB52919 and ABB52954-ABB53094) of nature
CC B2/D+A-. The polynucleotides have potential antiinflammatory,
CC antibacterial and immunosuppressive activity as part of pharmaceutical
CC compositions used to treat, palliate or prevent extra-intestinal E. coli
CC infections. The polypeptides are useful for determining the phylogenic
CC group of a given E. coli strain. These polypeptides can detect and treat
CC an undesired development of E. coli, particularly an extra-intestinal
CC infection that include systemic and non-diarrhoeal infections such as
CC septicaemia, pyelonephritis and meningitis this is particularly
CC advantageous as bacterial resistance is increasing with the more frequent
CC use of broad spectrum antibiotics
XX
SQ Sequence 611 AA;

Query Match 92.1%; Score 35; DB 4; Length 611;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NWGPLV 6
||||:|
Db 485 NWGPVV 490

RESULT 10
ABP04775
ID ABP04775 standard; protein; 51 AA.
XX
AC ABP04775;
XX
DT 24-JUN-2002 (first entry)
XX
DE Human ORFX protein sequence SEQ ID NO:9532.
XX
KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis.
XX
OS Homo sapiens.
XX
PN WO200192523-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US010836.
XX
PR 30-MAY-2000; 2000US-0206132P.
PR 29-AUG-2000; 2000US-0228716P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach MD;
XX
DR WPI; 2002-106308/14.
DR N-PSDB; ABN20527.
XX
PT Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders.
XX
PS Disclosure; SEQ ID NO 9532; 1037pp; English.
XX
CC The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a

CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage. N.B. The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 51 AA;

Query Match 89.5%; Score 34; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NWGPL 5
||||||
Db 7 NWGPL 11

RESULT 11
AAO12092
ID AAO12092 standard; protein; 59 AA.
XX
AC AAO12092;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 25984.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US004927.
XX
PR 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR N-PSDB; AAI92023.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX
PS Claim 20; SEQ ID NO 25984; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 59 AA;

Query Match 89.5%; Score 34; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NWGPL 5
||||||
Db 15 NWGPL 19

RESULT 12
ADM04268
ID ADM04268 standard; protein; 219 AA.
XX
AC ADM04268;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human protein of the invention SEQ ID NO:2953.
XX
KW human; gene therapy; diagnostic marker; pharmaceutical.
XX
OS Homo sapiens.
XX
PN EP1347046-A1.
XX
PD 24-SEP-2003.
XX
PF 12-APR-2002; 2002EP-00008400.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-723558/69.
DR N-PSDB; ADM01825.
XX
PT New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
PS Claim 1; SEQ ID NO 2953; 305pp; English.
XX
CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.
XX
SQ Sequence 219 AA;

Query Match 89.5%; Score 34; DB 7; Length 219;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 NWGPL 5
              |||||
Db         53 NWGPL 57


RESULT 13
ABB91948
ID   ABB91948 standard; protein; 250 AA.
XX
AC   ABB91948;
XX
DT   31-MAY-2002  (first entry)
XX
DE   Herbicidally active polypeptide SEQ ID NO 1159.
XX
KW   Herbicidal; plant; agriculture; herbicide.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200210210-A2.
XX
PD   07-FEB-2002.
XX
PF   28-AUG-2001; 2001WO-EP009892.
XX
PR   28-AUG-2001; 2001WO-EP009892.
XX
PA   (FARB ) BAYER AG.
XX
PI   Tietjen K,  Weidler M;
XX
DR   WPI; 2002-269010/31.
XX
PT   Identifying plant target proteins for herbicidally active compounds,
PT   comprising aligning and comparing nucleic acid or amino acid sequences
PT   from plant with nucleic acid or amino acid sequences from non-plant
PT   organisms.
XX
PS   Claim 5; SEQ ID NO 1159; 261pp + Sequence Listing; English.
XX
CC   The invention relates to identifying target proteins (ABB90790-ABB94016)
CC   for herbicidally active compounds, comprising aligning and comparing
CC   nucleic acid or amino acid sequences from plant with nucleic acid or
CC   amino acid sequences from non-plant organisms using suitable search
CC   parameters, where plant sequences having an E-value greater by a factor
CC   of 3 than the E-value of most similar non-plant sequences are selected.
CC   The polypeptides or nucleic acids encoding them are useful for
CC   identifying modulators. The identified modulators are useful as
CC   herbicides
XX
SQ   Sequence 250 AA;

  Query Match             89.5%;  Score 34;  DB 5;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NWGPL 5
              |||||
Db        209 NWGPL 213


RESULT 14
AAG43748
ID   AAG43748 standard; protein; 267 AA.
XX
AC   AAG43748;
XX
DT   18-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 54717.
XX
KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-00301439.
XX
PR   25-FEB-1999;   99US-0121825P.
PR   05-MAR-1999;   99US-0123180P.
PR   09-MAR-1999;   99US-0123548P.
PR   23-MAR-1999;   99US-0125788P.
PR   25-MAR-1999;   99US-0126264P.
PR   29-MAR-1999;   99US-0126785P.
PR   01-APR-1999;   99US-0127462P.
PR   06-APR-1999;   99US-0128234P.
PR   08-APR-1999;   99US-0128714P.
PR   16-APR-1999;   99US-0129845P.
PR   19-APR-1999;   99US-0130077P.
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PR   23-APR-1999;   99US-0130510P.
PR   23-APR-1999;   99US-0130891P.
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PR   30-APR-1999;   99US-0132048P.
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PR   05-MAY-1999;   99US-0132485P.
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PR   28-MAY-1999;   99US-0136782P.
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PR   23-JUN-1999;   99US-0140354P.
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PR 24-JUN-1999; 99US-0140695P.
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PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 89.5%; Score 34; DB 3; Length 267;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 NWGPL 5
              |||||
Db        226 NWGPL 230
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RESULT 15
AAG23820
ID AAG23820 standard; protein; 272 AA.
XX
AC AAG23820;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27267.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX

PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
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